



PCT10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/070,334

DATE: 08/13/2002

TIME: 16:38:23

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Output Set: N:\CRF4\08132002\J070334.raw

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3 <110> APPLICANT: WATANABE, TAKUYA
 4 KIKUCHI, KUNIKO
 5 SHINTANI, YASUSHI
 7 <120> TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR PROTEIN AND DNA
 8 THEREOF
 10 <130> FILE REFERENCE: 57126(46342)
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/070,334
 C--> 13 <141> CURRENT FILING DATE: 2002-07-12
 15 <150> PRIOR APPLICATION NUMBER: PCT/JP00/05683
 16 <151> PRIOR FILING DATE: 2000-08-08
 18 <150> PRIOR APPLICATION NUMBER: JP 11-241529
 19 <151> PRIOR FILING DATE: 1999-08-27
 21 <160> NUMBER OF SEQ ID NOS: 7
 23 <170> SOFTWARE: PatentIn Ver. 2.1
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 26 <211> LENGTH: 368
 27 <212> TYPE: PRT
 28 <213> ORGANISM: Homo sapiens
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 34 Gly Leu Ile Leu Ala Ala Val Val Glu Val Gly Ala Leu Leu Gly Asn
 35 20 25 30
 37 Gly Ala Leu Leu Val Val Val Leu Arg Thr Pro Gly Leu Arg Asp Ala
 38 35 40 45
 40 Leu Tyr Leu Ala His Leu Cys Val Val Asp Leu Leu Ala Ala Ala Ser
 41 50 55 60
 43 Ile Met Pro Leu Gly Leu Leu Ala Ala Pro Pro Pro Gly Leu Gly Arg
 44 65 70 75 80
 46 Val Arg Leu Gly Pro Ala Pro Cys Arg Ala Ala Arg Phe Leu Ser Ala
 47 85 90 95
 49 Ala Leu Leu Pro Ala Cys Thr Leu Gly Val Ala Ala Leu Gly Leu Ala
 50 100 105 110
 52 Arg Tyr Arg Leu Ile Val His Pro Leu Arg Pro Gly Ser Arg Pro Pro
 53 115 120 125
 55 Pro Val Leu Val Leu Thr Ala Val Trp Ala Ala Ala Gly Leu Leu Gly
 56 130 135 140
 58 Ala Leu Ser Leu Leu Gly Pro Pro Pro Ala Pro Pro Pro Ala Pro Ala
 59 145 150 155 160
 61 Arg Cys Ser Val Leu Ala Gly Gly Leu Gly Pro Phe Arg Pro Leu Trp
 62 165 170 175
 64 Ala Leu Leu Ala Phe Ala Leu Pro Ala Leu Leu Leu Leu Gly Ala Tyr
 65 180 185 190

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67 Gly Gly Ile Phe Val Val Ala Arg Arg Ala Ala Leu Arg Pro Pro Arg
68      195      200      205
70 Pro Ala Arg Gly Ser Arg Leu Arg Ser Asp Ser Leu Asp Ser Arg Leu
71      210      215      220
73 Ser Ile Leu Pro Pro Leu Arg Pro Arg Leu Pro Gly Gly Lys Ala Ala
74 225      230      235      240
76 Leu Ala Pro Ala Leu Ala Val Gly Gln Phe Ala Ala Cys Trp Leu Pro
77      245      250      255
79 Tyr Gly Cys Ala Cys Leu Ala Pro Ala Ala Arg Ala Ala Glu Ala Glu
80      260      265      270
82 Ala Ala Val Thr Trp Val Ala Tyr Ser Ala Phe Ala Ala His Pro Phe
83      275      280      285
85 Leu Tyr Gly Leu Leu Gln Arg Pro Val Arg Leu Ala Leu Gly Arg Leu
86      290      295      300
88 Ser Arg Arg Ala Leu Pro Gly Pro Val Arg Ala Cys Thr Pro Gln Ala
89 305      310      315      320
91 Trp His Pro Arg Ala Leu Leu Gln Cys Leu Gln Arg Pro Pro Glu Gly
92      325      330      335
94 Pro Ala Val Gly Pro Ser Glu Ala Pro Glu Gln Thr Pro Glu Leu Ala
95      340      345      350
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147 <222> LOCATION: (2084)
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165 gggcagccaa tgaggtgagg ggccggagga gcaagggaca agaggagcag aggacaggtg 180
167 atggaaatcc tgcagcttta ggctccattc tgccatctac atcccagcgc aggggtgaagc 240
169 ctgagagccc aa atg gcc aac tcc aca ggg ctg aac gcc tca gaa gtc gca 291
170 Met Ala Asn Ser Thr Gly Leu Asn Ala Ser Glu Val Ala
171 1 5 10
173 ggc tcg ttg ggg ttg atc ctg gca gct gtc gtg gag gtg ggg gca ctg 339
174 Gly Ser Leu Gly Leu Ile Leu Ala Ala Val Val Glu Val Gly Ala Leu
175 15 20 25
177 ctg ggc aac ggc gcg ctg ctg gtc gtg gtg ctg cgc acg ccg gga ctg 387
178 Leu Gly Asn Gly Ala Leu Leu Val Val Val Leu Arg Thr Pro Gly Leu
179 30 35 40 45
181 cgc gac gcg ctc tac ctg gcg cac ctg tgc gtc gtg gac ctg ctg gcg 435
182 Arg Asp Ala Leu Tyr Leu Ala His Leu Cys Val Val Asp Leu Leu Ala
183 50 55 60
185 gcc gcc tcc atc atg ccg ctg ggc ctg ctg gcc gca ccg ccg gcc ggg 483
186 Ala Ala Ser Ile Met Pro Leu Gly Leu Leu Ala Ala Pro Pro Pro Gly
187 65 70 75
189 ctg ggc cgc gtg cgc ctg ggc ccc gcg cca tgc cgc gcc gct cgc ttc 531
190 Leu Gly Arg Val Arg Leu Gly Pro Ala Pro Cys Arg Ala Ala Arg Phe
191 80 85 90
193 ctc tcc gcc gct ctg ctg ccg gcc tgc acg ctc ggg gtg gcc gca ctt 579
194 Leu Ser Ala Ala Leu Leu Pro Ala Cys Thr Leu Gly Val Ala Ala Leu
195 95 100 105
197 ggc ctg gca cgc tac cgc ctc atc gtg cac ccg ctg cgg cca ggc tcg 627
198 Gly Leu Ala Arg Tyr Arg Leu Ile Val His Pro Leu Arg Pro Gly Ser
199 110 115 120 125

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201 cgg ccg ccg cct gtg ctc gtg ctc acc gcc gtg tgg gcc gcg gcg gga 675
202 Arg Pro Pro Pro Val Leu Val Leu Thr Ala Val Trp Ala Ala Ala Gly
203 130 135 140
205 ctg ctg ggc gcg ctc tcc ctg ctc ggc ccg ccg ccc gca ccg ccc cct 723
206 Leu Leu Gly Ala Leu Ser Leu Leu Gly Pro Pro Pro Ala Pro Pro Pro
207 145 150 155
209 gct cct gct cgc tgc tgc gtc ctg gct ggg ggc ctc ggg ccc ttc cgg 771
210 Ala Pro Ala Arg Cys Ser Val Leu Ala Gly Gly Leu Gly Pro Phe Arg
211 160 165 170
213 ccg ctc tgg gcc ctg ctg gcc ttc gcg ctg ccc gcc ctc ctg ctg ctc 819
214 Pro Leu Trp Ala Leu Leu Ala Phe Ala Leu Pro Ala Leu Leu Leu Leu
215 175 180 185
217 ggc gcc tac ggc ggc atc ttc gtg gtg gcg cgt cgc gct gcc ctg agg 867
218 Gly Ala Tyr Gly Gly Ile Phe Val Val Ala Arg Arg Ala Ala Leu Arg
219 190 195 200 205
221 ccc cca cgg ccg gcg cgc ggg tcc cga ctc cgc tcg gac tct ctg gat 915
222 Pro Pro Arg Pro Ala Arg Gly Ser Arg Leu Arg Ser Asp Ser Leu Asp
223 210 215 220
225 agc cgc ctt tcc atc ttg ccg ccg ctc cgg cct cgc ctg ccc ggg ggc 963
226 Ser Arg Leu Ser Ile Leu Pro Pro Leu Arg Pro Arg Leu Pro Gly Gly
227 225 230 235
229 aag gcg gcc ctg gcc cca gcg ctg gcc gtg ggc caa ttt gca gcc tgc 1011
230 Lys Ala Ala Leu Ala Pro Ala Leu Ala Val Gly Gln Phe Ala Ala Cys
231 240 245 250
233 tgg ctg cct tat ggc tgc gcg tgc ctg gcg ccc gca gcg cgg gcc gcg 1059
234 Trp Leu Pro Tyr Gly Cys Ala Cys Leu Ala Pro Ala Ala Arg Ala Ala
235 255 260 265
237 gaa gcc gaa gcg gct gtc acc tgg gtc gcc tac tcg gcc ttc gcg gct 1107
238 Glu Ala Glu Ala Ala Val Thr Trp Val Ala Tyr Ser Ala Phe Ala Ala
239 270 275 280 285
241 cac ccc ttc ctg tac ggg ctg ctg cag cgc ccc gtg cgc ttg gca ctg 1155
242 His Pro Phe Leu Tyr Gly Leu Leu Gln Arg Pro Val Arg Leu Ala Leu
243 290 295 300
245 ggc cgc ctc tct cgc cgt gca ctg cct gga cct gtg cgg gcc tgc act 1203
246 Gly Arg Leu Ser Arg Arg Ala Leu Pro Gly Pro Val Arg Ala Cys Thr
247 305 310 315
249 ccg caa gcc tgg cac ccg cgg gca ctc ttg caa tgc ctc cag aga ccc 1251
250 Pro Gln Ala Trp His Pro Arg Ala Leu Leu Gln Cys Leu Gln Arg Pro
251 320 325 330
253 cca gag ggc cct gcc gta ggc cct tct gag gct cca gaa cag acc ccc 1299
254 Pro Glu Gly Pro Ala Val Gly Pro Ser Glu Ala Pro Glu Gln Thr Pro
255 335 340 345
257 gag ttg gca gga ggg cgg agc ccc gca tac cag ggg cca cct gag agt 1347
258 Glu Leu Ala Gly Gly Arg Ser Pro Ala Tyr Gln Gly Pro Pro Glu Ser
259 350 355 360 365
261 tct ctc tcc tgagcaggag aaaggagggt ggtttccgtg ggggctcatc 1396
262 Ser Leu Ser
264 caaccctgc acagggtcaca gcagggtgccc tgctggatat ctgggtctg aacaggagga 1456
266 gaaagggtgt ctgctgcctg gtgaggccca cggacttctg agagccagga atcctgcggt 1516

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268 ctggggcccaa cactgcatag cactgtgcat aggccgaccc ttccttaggc ctcagctttc 1576
270 ccatctgcac cctgcagcat ctctaagggc ccctccagca taggtgggtt gtgaaactca 1636
272 caggtggtcc ccaggccaag atgggcaggt gtcacaaaga agagggccct aagggtcac 1696
274 aaccaaagt atccgccaag cagggcagta tctgggttac agccacagca ggaagaacca 1756
276 ctggagacac actcagaagg acttccctga catctgcacc aaggagagtc tggacaaagc 1816
278 tactgaaact cctccacctg cttctaaaat gcccagaaga caactggacc agtttggtat 1876
280 tagaagtagg aggctggacg acttcacccc caaaggggtcc tgaagcccca gaactggcat 1936
282 gtggaagggg gtgaggccca attgaggttg gtggattcac acatgggggt cctccaggcc 1996
W--> 284 ctcagctgcc cccatttttt ggnggttttg ctgccccan cccagnttt tcncaacttc 2056
W--> 286 ctggtcgctg agaatttttn ttcaaaancca gggnttgaaa nncctgaaaa aaaaaaaaaa 2116
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306 <213> ORGANISM: Artificial Sequence
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311 <400> SEQUENCE: 4
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315 <210> SEQ ID NO: 5
316 <211> LENGTH: 20
317 <212> TYPE: DNA
318 <213> ORGANISM: Artificial Sequence
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340 <211> LENGTH: 21
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342 <213> ORGANISM: Artificial Sequence
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345 <223> OTHER INFORMATION: Description of Artificial Sequence: Probe

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/070,334

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Input Set : A:\57146342.app
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; N Pos. 102,2019,2036,2044,2049,2072,2076,2084,2090,2097,2098